

Genome-wide association study of weight gain in feedlot Nellore cattle: comparison of single nucleotide polymorphism and haplotype blocks approaches

Adriana L. Somavilla^{*1}, Marcílio D. S. Mota², Antonio N. Rosa³, Luiz L. Coutinho^{4,6},
Mauricio M. Alencar^{5,6}, Rymer R. Tullio⁵, Mauricio A. Mudadu⁵, Luciana C. A.
Regitano^{5,6}

^{*} PhD student, Unesp/Fcav; Via de Acesso Prof. Paulo Donato Castellane s/n;
Jaboticabal, SP 14884-900 Brazil;

¹Universidade Estadual Paulista, Fcav, Jaboticabal, SP; ²Universidade Estadual Paulista, Botucatu, SP; ³Embrapa Gado de Corte, Campo Grande, MS; ⁴Escola Superior de Agricultura Luiz de Queiroz, Piracicaba, SP; ⁵Embrapa Pecuária Sudeste, São Carlos, SP; ⁶Pesquisador CNPq

* adri_somavilla@yahoo.com.br

The search for animals with higher growth rates could result in a shorter production cycle, with animals remaining less time in feedlot and improvement of the production system. Weight gain is one easy to measure trait that can be used as selection criterion. Genome-wide association studies have been used to identify quantitative trait loci (QTL) associated with complex traits and this can be useful to know what genes control the traits and to increase the accuracy of selection in breeding programs. However, depending on the extension of linkage disequilibrium, a single SNP association may be neglected. In this case, haplotype-based analysis is expected to detect it. Data from 762 heifers, descendants from 34 Nellore sires were used to prediction of their breeding values (EBVs). The MTDFREML software under an animal model was used to perform the analysis. The effect of the contemporary group was considered as fixed and the linear effects of days in feedlot and slaughter age were included as covariates. The EBVs for the trait weight gain in feedlot period were defined as the phenotype for further analysis. After filtering individuals call rate (95%), minor allele frequency (5%) and Hardy-Weinberg equilibrium deviations ($P < 0.001$), 334,080 single nucleotide polymorphisms (SNPs) from the Illumina BovineHD BeadChip and 788 individuals remained. The haplotype reconstructions, single SNPs and haplotype association analyses were performed by the software Plink that implements Wald test and Bonferroni correction. In the single SNP approach, five chromosomal regions containing significant adjacent SNPs were observed: BTA 6 (118.52 to 118.58 Mb), 9 (98.4 to 98.5 Mb), 10 (65.4 to 65.6 Mb), 23 (11.04 to 11.3 Mb) and 29 (37.5 to 37.8 Mb). On the haplotype approach, five genomic regions were also identified: BTA 6 (112.7 to 118.5 Mb), 18 (3.4 to 5.7 Mb), 23 (21.8 to 24.4 MB) and 29 (37.5 to 37.8 Mb). The regions on BTA 6 are near QTLs for growth traits. On BTA 9 segment was found a gene related to growth and development (MAP3K4). BTA 23 showed two important regions, the one from SNP-based analysis, which is near QTLs for slaughter weight and the other one lying inside a QTL for birth weight. The last common segment is on BTA 29, that contains QTLs for meat quality, but they are non-overlapping the region found in this study. Both approaches allowed the identification of previously described and new QTLs for the trait, as the ones on BTA 10 and 18. Our results suggest that the EBVs for weight gain in feedlot period can be used as phenotype in association analysis and it suggests the existence of genetic variation in this population, which was important to identify genomic regions associated to the studied trait. Furthermore, to compare SNPs and haplotype approaches it might be useful to explore the genes on QTL regions..

Keywords: beef cattle, *Bos indicus*, growth, QTL, SNP

Acknowledgments: The authors thank Fundação de Apoio à Pesquisa do Estado de São Paulo (FAPESP) for providing scholarship to Somavilla and Embrapa Pecuária Sudeste for financial support.